



SEQUENCE LISTING

#9

<110> Houtzager, Erwin
Vijn, Irma Maria Caecilia
Sijmons, Peter Christiaan

<120> A Structure for Presenting Desired Peptide Sequences

<130> 2183-5208US

<140> US 10,016,516
<141> 2001-12-10

<160> 24

<170> PatentIn version 3.1

<210> 1
<211> 291
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: 5' end of exemplary maximal
primary scaffold

<220>
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<222> (79)..(93)
<223> The nucleotide at each of positions 79-93 is unknown

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<223> The nucleotide at each of positions 157-159 is unknown

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<400> 1
aat gtg aaa ctg gtt gaa aaa ggt ggc aat ttc gtc gaa aac gat gac 48
Ala Val Lys Leu Val Glu Lys Gly Gly Asn Phe Val Glu Asn Asp Asp
1 5 10 15

gat ctt aag ctg acg tgc cgt gct gaa ggt nnn nnn nnn nnn nnn tac 96
Asp Leu Lys Leu Thr Cys Arg Ala Glu Gly Xaa Xaa Xaa Xaa Xaa Tyr
20 25 30

tgc atg ggt tgg ttc cgt cag gcg ccg aac gac gac agt act aac gtg 144
Cys Met Gly Trp Phe Arg Gln Ala Pro Asn Asp Asp Ser Thr Asn Val

35 40 45
 gcc acg atc tta nnn ggg agc acg tac tac ggt gac tcc gtc aaa gag 192
 Ala Thr Ile Leu Xaa Gly Ser Thr Tyr Tyr Gly Asp Ser Val Lys Glu
 50 55 60
 cgc ttc gat atc cgt cgc gac nnn nnn nnn aac acc gtt acc tta tcg 240
 Arg Phe Asp Ile Arg Arg Asp Xaa Xaa Xaa Asn Thr Val Thr Leu Ser
 65 70 75 80
 atg gac gat ctg caa ccg gaa gac tct gca gaa tac aat tgt gca ggt 288
 Met Asp Asp Leu Gln Pro Glu Asp Ser Ala Glu Tyr Asn Cys Ala Gly
 85 90 95
 tct 291
 Ser

<210> 2
 <211> 97
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: 5' end of exemplary maximal
 primary scaffold

<220>
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 <222> (27)..(31)
 <223> The amino acid at each of positions 27-31 is unknown

<220>
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 <223> The amino acid at position 53 is unknown

<220>
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 <223> The amino acid at each of positions 72-74 is unknown

<400> 2

Ala Val Lys Leu Val Glu Lys Gly Gly Asn Phe Val Glu Asn Asp Asp
 1 5 10 15

Asp Leu Lys Leu Thr Cys Arg Ala Glu Gly Xaa Xaa Xaa Xaa Xaa Tyr
 20 25 30

Cys Met Gly Trp Phe Arg Gln Ala Pro Asn Asp Asp Ser Thr Asn Val
 35 40 45

Ala Thr Ile Leu Xaa Gly Ser Thr Tyr Tyr Gly Asp Ser Val Lys Glu
 50 55 60

Arg Phe Asp Ile Arg Arg Asp Xaa Xaa Xaa Asn Thr Val Thr Leu Ser
 65 70 75 80

Met Asp Asp Leu Gln Pro Glu Asp Ser Ala Glu Tyr Asn Cys Ala Gly
 85 90 95

Ser

<210> 3
 <211> 42
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: 3' end of exemplary maximal
 primary scaffold

<400> 3
 tac cac tac cgt ggt cag ggt acc gac gtt acc gtc tcg tcg 42
 Tyr His Tyr Arg Gly Gln Gly Thr Asp Val Thr Val Ser Ser
 1 5 10

<210> 4
 <211> 14
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: 3' end of exemplary maximal
 primary scaffold

<400> 4

Tyr His Tyr Arg Gly Gln Gly Thr Asp Val Thr Val Ser Ser
 1 5 10

<210> 5
 <211> 17
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: T7 primer

<400> 5
aatacgactc actatag

17

<210> 6
<211> 17
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: T3 primer

<400> 6
attaaccctc actaaag

17

<210> 7
<211> 125
<212> PRT
<213> Lama

<220>
<221> SITE
<222> (1)..(125)
<223> IF2X-single domain camelid antibody Cab-Ca05

<400> 7

Gln Val Gln Leu Val Glu Ser Gly Gly Gly Ser Val Gln Ala Gly Gly
1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Tyr Thr Val Ser Thr Tyr
20 25 30

Cys Met Gly Trp Phe Arg Gln Ala Pro Gly Lys Glu Arg Glu Gly Val
35 40 45

Ala Thr Ile Leu Gly Gly Ser Thr Tyr Tyr Gly Asp Ser Val Lys Gly
50 55 60

Arg Phe Thr Ile Ser Gln Asp Asn Ala Lys Asn Thr Val Tyr Leu Gln
65 70 75 80

Met Asn Ser Leu Lys Pro Glu Asp Thr Ala Ile Tyr Tyr Cys Ala Gly
85 90 95

Ser Thr Val Ala Ser Thr Gly Trp Cys Ser Arg Leu Arg Pro Tyr Asp
100 105 110

Tyr His Tyr Arg Gly Gln Gly Thr Gln Val Thr Val Ser
 115 120 125

<210> 8
 <211> 127
 <212> PRT
 <213> Lama

<220>
 <221> SITE
 <222> (1)..(127)
 <223> 1QD0-camelid heavy chain variable domain

<400> 8

Gln Val Gln Leu Gln Glu Ser Gly Gly Gly Leu Val Gln Ala Gly Gly
 1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Arg Ala Ala Ser Gly His
 20 25 30

Gly His Tyr Gly Met Gly Trp Phe Arg Gln Val Pro Gly Lys Glu Arg
 35 40 45

Glu Phe Val Ala Ala Ile Arg Trp Ser Gly Lys Glu Thr Trp Tyr Lys
 50 55 60

Asp Ser Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Thr
 65 70 75 80

Thr Val Tyr Leu Gln Met Asn Ser Leu Lys Gly Glu Asp Thr Ala Val
 85 90 95

Tyr Tyr Cys Ala Ala Arg Pro Val Arg Val Ala Asp Ile Ser Leu Pro
 100 105 110

Val Gly Phe Asp Tyr Trp Gly Gln Gly Thr Gln Val Thr Val Ser
 115 120 125

<210> 9
 <211> 120
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SITE
 <222> (1)..(120)
 <223> 8FAB-heavy chain from human Iggl

<400> 9

Ala Val Lys Leu Val Gln Ala Gly Gly Gly Val Val Gln Pro Gly Arg
 1 5 10 15

Ser Leu Arg Leu Ser Cys Ile Ala Ser Gly Phe Thr Phe Ser Asn Tyr
 20 25 30

Gly Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
 35 40 45

Ala Val Ile Trp Tyr Asn Gly Ser Arg Thr Tyr Tyr Gly Asp Ser Val
 50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Arg Thr Leu Tyr
 65 70 75 80

Met Gln Met Asn Ser Leu Arg Thr Glu Asp Thr Ala Val Tyr Tyr Cys
 85 90 95

Ala Arg Asp Pro Asp Ile Leu Thr Ala Phe Ser Phe Asp Tyr Trp Gly
 100 105 110

Gln Gly Val Leu Val Thr Val Ser
 115 120

<210> 10
 <211> 89
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SITE
 <222> (11)..(89)
 <223> 1VSC - Vcam-1

<400> 10

Phe Lys Ile Glu Thr Thr Pro Glu Ser Arg Tyr Leu Ala Gln Ile Gly

1 5 10 15
 Asp Ser Val Ser Leu Thr Cys Ser Thr Thr Gly Cys Glu Ser Pro Phe
 20 25 30
 Phe Ser Trp Arg Thr Gln Ile Asp Ser Pro Leu Asn Gly Lys Val Thr
 35 40 45
 Asn Glu Gly Thr Thr Ser Thr Leu Thr Met Asn Pro Val Ser Phe Gly
 50 55 60
 Asn Glu His Ser Tyr Leu Cys Thr Ala Thr Cys Glu Ser Arg Lys Leu
 65 70 75 80
 Glu Lys Gly Ile Gln Val Glu Ile Tyr
 85

<210> 11
 <211> 92
 <212> PRT
 <213> Hepatitis C virus

<220>
 <221> SITE
 <222> (1)..(92)
 <223> 1NS3 - structure of Hcv Protease (Bk strain)

<400> 11
 Thr Gln Ser Phe Leu Ala Thr Cys Val Asn Gly Val Cys Trp Thr Val
 1 5 10 15
 Tyr His Gly Ala Gly Ser Lys Thr Leu Ala Gly Pro Lys Gly Pro Ile
 20 25 30
 Thr Gly Met Tyr Thr Asn Val Asp Gln Asp Leu Val Gly Trp Gln Ala
 35 40 45
 Pro Pro Gly Ala Arg Ser Leu Thr Pro Cys Thr Cys Gly Ser Ser Asp
 50 55 60
 Leu Tyr Leu Val Thr Arg His Ala Asp Val Ile Pro Val Arg Arg Arg
 65 70 75 80

Gly Asp Ser Arg Gly Ser Leu Leu Ser Pro Arg Pro
85 90

<210> 12
<211> 102
<212> PRT
<213> Mus musculus

<220>
<221> SITE
<222> (1)..(102)
<223> 1F97 - soluble part of the junction adhesion molecule

<400> 12

Lys Gly Ser Val Tyr Thr Ala Gln Ser Asp Val Gln Val Pro Glu Asn
1 5 10 15

Glu Ser Ile Lys Leu Thr Cys Thr Tyr Ser Gly Phe Ser Ser Pro Arg
20 25 30

Val Glu Trp Lys Phe Val Gln Gly Ser Thr Thr Ala Leu Val Cys Tyr
35 40 45

Asn Ser Gln Ile Thr Ala Pro Tyr Ala Asp Arg Val Thr Phe Ser Ser
50 55 60

Ser Gly Ile Thr Phe Ser Ser Val Thr Arg Lys Asp Asn Gly Glu Tyr
65 70 75 80

Thr Cys Met Val Ser Glu Glu Gly Gly Gln Asn Tyr Gly Glu Val Ser
85 90 95

Ile His Leu Thr Val Leu
100

<210> 13
<211> 91
<212> PRT
<213> Homo sapiens

<220>
<221> SITE
<222> (1)..(91)
<223> IFNF - fragment of fibronectin encompassing type-III repeats 7 th

rough 10

<400> 13

Val Pro Pro Pro Thr Asp Leu Arg Thr Thr Asn Ile Gly Pro Asp Thr
1 5 10 15

His Arg Val Thr Trp Ala Pro Pro Pro Ser Ile Asp Leu Thr Asn Phe
20 25 30

Leu Val Arg Tyr Ser Pro Val Lys Met Glu Glu Asp Val Ala Glu Leu
35 40 45

Ser Ile Ser Pro Ser Asp Asn Ala Val Val Leu Thr Asn Leu Leu Pro
50 55 60

Gly Thr Glu Tyr Val Val Ser Val Ser Ser Val Tyr Glu Gln His Glu
65 70 75 80

Ser Thr Pro Leu Arg Gly Arg Glu Lys Thr Gly
85 90

<210> 14

<211> 95

<212> PRT

<213> Drosophila

<220>

<221> SITE

<222> (1)..(95)

<223> neuroglial

<400> 14

Pro Asn Ala Pro Lys Leu Thr Gly Ile Thr Cys Gln Ala Asp Lys Ala
1 5 10 15

Glu Ile His Trp Glu Gln Gln Gly Asp Asn Arg Ser Pro Ile Leu His
20 25 30

Tyr Thr Ile Gln Phe Asn Thr Ser Phe Thr Pro Ala Ser Trp Asp Ala
35 40 45

Ala Tyr Glu Lys Val Pro Asn Thr Asp Ser Ser Phe Val Val Gln Met

50

55

60

Ser Pro Trp Ala Asn Tyr Thr Phe Arg Val Ile Ala Phe Asn Lys Ile
 65 70 75 80

Gly Ala Ser Pro Pro Ser Ala His Ser Asp Ser Cys Thr Thr Gln
 85 90 95

<210> 15
 <211> 100
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SITE
 <222> (1)..(100)
 <223> 1IAR - interleukin-4 receptor alpha chain complex

<400> 15

Arg Ala Pro Gly Asn Leu Thr Val His Thr Asn Val Ser Asp Thr Leu
 1 5 10 15

Leu Leu Thr Trp Ser Asn Pro Tyr Pro Pro Asp Asn Tyr Leu Tyr Asn
 20 25 30

His Leu Thr Tyr Ala Val Asn Ile Ser Glu Asn Asp Pro Ala Asp Glu
 35 40 45

Arg Ile Tyr Asn Val Thr Tyr Leu Glu Pro Ser Leu Arg Ile Ala Ala
 50 55 60

Ser Thr Leu Lys Ser Gly Ile Ser Tyr Arg Ala Arg Val Arg Ala Trp
 65 70 75 80

Ala Gln Ala Tyr Asn Thr Thr Trp Ser Glu Trp Ser Pro Ser Thr Lys
 85 90 95

Trp His Asn Ala
 100

<210> 16
 <211> 100
 <212> PRT

<213> Escherichia coli

<220>

<221> SITE

<222> (1)..(100)

<223> 1F4H (Lacz) beta-galactosidase (orthorhombic)

<400> 16

Phe Phe Gln Phe Arg Leu Ser Gly Gln Thr Ile Glu Val Thr Ser Glu
1 5 10 15

Tyr Leu Phe Arg His Ser Asp Asn Glu Leu Leu His Trp Met Val Ala
20 25 30

Leu Asp Gly Lys Pro Leu Ala Ser Gly Glu Val Pro Ile Asp Val Ala
35 40 45

Pro Gln Gly Lys Gln Leu Ile Glu Leu Pro Glu Leu Pro Gly Pro Glu
50 55 60

Ser Ala Gly Gln Leu Trp Leu Thr Val Arg Val Val Gln Pro Asn Ala
65 70 75 80

Thr Ala Trp Ser Glu Ala Gly His Ile Ser Ala Trp Gln Gln Trp Arg
85 90 95

Leu Ala Glu Asn
100

<210> 17

<211> 405

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Scaffold with Vhh 1MEL CDR regions

<400> 17

aat gtg aaa ctg gtt gaa aaa ggt ggc aat ttc gtc gaa aac gat gac 48
Asn Val Lys Leu Val Glu Lys Gly Gly Asn Phe Val Glu Asn Asp Asp
1 5 10 15

gat ctt aag ctc acg tgc cgt gct gaa ggt tac acc att ggc ccg tac 96
Asp Leu Lys Leu Thr Cys Arg Ala Glu Gly Tyr Thr Ile Gly Pro Tyr
20 25 30

tgc atg ggt tgg ttc cgt cag gcg ccg aac gac gac agt act aac gtg 144
 Cys Met Gly Trp Phe Arg Gln Ala Pro Asn Asp Asp Ser Thr Asn Val
 35 40 45

gcc acg atc aac atg ggt ggc ggt att acg tac tac ggt gac tcc gtc 192
 Ala Thr Ile Asn Met Gly Gly Gly Ile Thr Tyr Tyr Gly Asp Ser Val
 50 55 60

aaa gag cgc ttc gat atc cgt cgc gac aac gcg tcc aac acc gtt acc 240
 Lys Glu Arg Phe Asp Ile Arg Arg Asp Asn Ala Ser Asn Thr Val Thr
 65 70 75 80

tta tcg atg gac gat ctg caa ccg gaa gac tct gca gaa tac aat tgt 288
 Leu Ser Met Asp Asp Leu Gln Pro Glu Asp Ser Ala Glu Tyr Asn Cys
 85 90 95

gca ggt gat tct acc att tac gcg agc tat tat gaa tgt ggt cat ggc 336
 Ala Gly Asp Ser Thr Ile Tyr Ala Ser Tyr Tyr Glu Cys Gly His Gly
 100 105 110

ctg agt acc ggc ggt tac ggc tac gat agc cac tac cgt ggt cag ggt 384
 Leu Ser Thr Gly Gly Tyr Gly Tyr Asp Ser His Tyr Arg Gly Gln Gly
 115 120 125

acc gac gtt acc gtc tcg tcg 405
 Thr Asp Val Thr Val Ser Ser
 130 135

<210> 18
 <211> 135
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Scaffold with Vhh 1MEL CDR regions

<400> 18

Asn Val Lys Leu Val Glu Lys Gly Gly Asn Phe Val Glu Asn Asp Asp
 1 5 10 15

Asp Leu Lys Leu Thr Cys Arg Ala Glu Gly Tyr Thr Ile Gly Pro Tyr
 20 25 30

Cys Met Gly Trp Phe Arg Gln Ala Pro Asn Asp Asp Ser Thr Asn Val
 35 40 45

Ala Thr Ile Asn Met Gly Gly Gly Ile Thr Tyr Tyr Gly Asp Ser Val
 50 55 60

Lys Glu Arg Phe Asp Ile Arg Arg Asp Asn Ala Ser Asn Thr Val Thr
 65 70 75 80

Leu Ser Met Asp Asp Leu Gln Pro Glu Asp Ser Ala Glu Tyr Asn Cys
 85 90 95

Ala Gly Asp Ser Thr Ile Tyr Ala Ser Tyr Tyr Glu Cys Gly His Gly
 100 105 110

Leu Ser Thr Gly Gly Tyr Gly Tyr Asp Ser His Tyr Arg Gly Gln Gly
 115 120 125

Thr Asp Val Thr Val Ser Ser
 130 135

<210> 19
 <211> 363
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Scaffold with Vhh 1BZQ CDR regions

<400> 19
 aat gtg aaa ctg gtt gaa aaa ggt ggc aat ttc gtc gaa aac gat gac 48
 Asn Val Lys Leu Val Glu Lys Gly Gly Asn Phe Val Glu Asn Asp Asp
 1 5 10 15

gat ctt aag ctg acg tgc cgt gct agc ggt tac gcc tac acg tat atc 96
 Asp Leu Lys Leu Thr Cys Arg Ala Ser Gly Tyr Ala Tyr Thr Tyr Ile
 20 25 30

tac atg ggt tgg ttc cgt cag gcg ccg aac gac gac agt act aac gtg 144
 Tyr Met Gly Trp Phe Arg Gly Ala Pro Asn Asp Asp Ser Thr Asn Val
 35 40 45

gcc acc atc gac tcg ggt ggc ggc ggt acc ctg tac ggt gac tcc gtc 192
 Ala Thr Ile Asp Ser Gly Gly Gly Thr Leu Tyr Gly Asp Ser Val
 50 55 60

aaa gag cgc ttc gat atc cgt cgc gac aaa ggc tcc aac acc gtt acc 240
 Leu Glu Arg Phe Asp Ile Arg Arg Asp Lys Gly Ser Asn Thr Val Thr
 65 70 75 80

tta tcg atg gac gat ctg caa ccg gaa gac tct gca gaa tac aat tgt 288

Leu Ser Met Asp Asp Leu Glu Pro Glu Asp Ser Ala Glu Tyr Asn Cys
85 90 95

gca gcg ggt ggc tac gaa ctg cgc gac cgc acc tac ggt cag cgt ggt 336
Ala Ala Gly Gly Tyr Glu Leu Arg Asp Arg Thr Tyr Gly Glu Arg Gly
100 105 110

cag ggt acc gac gtt acc gtc tcg tcg 363
Glu Gly Thr Asp Val Thr Val Ser Ser
115 120

<210> 20
<211> 121
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Scaffold with Vhh 1BZQ CDR
regions

<400> 20

Asn Val Lys Leu Val Glu Lys Gly Gly Asn Phe Val Glu Asn Asp Asp
1 5 10 15

Asp Leu Lys Leu Thr Cys Arg Ala Ser Gly Tyr Ala Tyr Thr Tyr Ile
20 25 30

Tyr Met Gly Trp Phe Arg Gly Ala Pro Asn Asp Asp Ser Thr Asn Val
35 40 45

Ala Thr Ile Asp Ser Gly Gly Gly Gly Thr Leu Tyr Gly Asp Ser Val
50 55 60

Leu Glu Arg Phe Asp Ile Arg Arg Asp Lys Gly Ser Asn Thr Val Thr
65 70 75 80

Leu Ser Met Asp Asp Leu Glu Pro Glu Asp Ser Ala Glu Tyr Asn Cys
85 90 95

Ala Ala Gly Gly Tyr Glu Leu Arg Asp Arg Thr Tyr Gly Glu Arg Gly
100 105 110

Glu Gly Thr Asp Val Thr Val Ser Ser
115 120

<210> 21

<211> 351
<212> DNA
<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Scaffold with Vhh 1HCV CDR regions

<400> 21

aat gtg aaa ctg gtt gaa aaa ggt ggc aat ttc gtc gaa aac gat gac 48
Asn Val Lys Leu Val Glu Lys Gly Gly Asn Phe Val Glu Asn Asp Asp
1 5 10 15

gat ctt aag ctc acg tgc cgt gct gaa ggt cgt acg ggt tcg acc tac 96
Asp Leu Lys Leu Thr Cys Arg Ala Glu Gly Arg Thr Gly Ser Thr Tyr
20 25 30

gat atg ggt tgg ttc cgt cag gcg ccg aac gac gac agt act aac gtg 144
Asp Met Gly Trp Phe Arg Gln Ala Pro Asn Asp Asp Ser Thr Asn Val
35 40 45

gcc acg atc aac tgg gat agc gcc cgt acg tac tac ggt gac tcc gtc 192
Ala Thr Ile Asn Trp Asp Ser Ala Arg Thr Tyr Tyr Gly Asp Ser Val
50 55 60

aaa gag cgc ttc gat atc cgt cgc gac aat gcc tcc aac acc gtt acc 240
Lys Glu Arg Phe Asp Ile Arg Arg Asp Asn Ala Ser Asn Thr Val Thr
65 70 75 80

tta tcg atg gac gat ctg caa ccg gaa gac tct gca gaa tac aat tgt 288
Leu Ser Met Asp Asp Leu Gln Pro Glu Asp Ser Ala Glu Tyr Asn Cys
85 90 95

gca ggt ggt gaa ggc ggc acc tgg gat agc cgt ggt cag ggt acc gac 336
Ala Gly Gly Glu Gly Gly Arg Trp Asp Ser Arg Gly Gln Gly Thr Asp
100 105 110

gtt acc gtc tcg tcg 351
Val Thr Val Ser Ser
115

<210> 22
<211> 117
<212> PRT
<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Scaffold with Vhh 1HCV CDR regions

<400> 22

Asn Val Lys Leu Val Glu Lys Gly Gly Asn Phe Val Glu Asn Asp Asp
1 5 10 15

Asp Leu Lys Leu Thr Cys Arg Ala Glu Gly Arg Thr Gly Ser Thr Tyr
 20 25 30

Asp Met Gly Trp Phe Arg Gln Ala Pro Asn Asp Asp Ser Thr Asn Val
 35 40 45

Ala Thr Ile Asn Trp Asp Ser Ala Arg Thr Tyr Tyr Gly Asp Ser Val
 50 55 60

Lys Glu Arg Phe Asp Ile Arg Arg Asp Asn Ala Ser Asn Thr Val Thr
 65 70 75 80

Leu Ser Met Asp Asp Leu Gln Pro Glu Asp Ser Ala Glu Tyr Asn Cys
 85 90 95

Ala Gly Gly Glu Gly Gly Arg Trp Asp Ser Arg Gly Gln Gly Thr Asp
 100 105 110

Val Thr Val Ser Ser
 115

<210> 23
 <211> 363
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Exemplary primary scaffold

<220>
 <221> misc_feature
 <222> (73)..(99)
 <223> The nucleotide at positions 73-99 is unknown

<220>
 <221> misc_feature
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 <223> The nucleotide at positions 157-177 is unknown

<220>
 <221> misc_feature
 <222> (292)..(333)
 <223> The nucleotide at positions 292-333 is unknown


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<400> 23
aat gtg aaa ctg gtt gaa aaa ggt ggc aat ttc gtc gaa aac gat gac 48
Asn Val Lys Leu Val Glu Lys Gly Gly Asn Phe Val Glu Asn Asp Asp
1 5 10 15

gat ctt aag ctc acg tgc cgt gct nnn nnn nnn nnn nnn nnn nnn nnn 96
Asp Leu Lys Leu Thr Cys Arg Ala Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
20 25 30

nnn atg ggt tgg ttc cgt cag gcg ccg aac gac gac agt act aac gtg 144
Xaa Met Gly Trp Phe Arg Gln Ala Pro Asn Asp Asp Ser Thr Asn Val
35 40 45

gcc acc atc gac nnn nnn nnn nnn nnn nnn nnn tac ggt gac tcc gtc 192
Ala Thr Ile Asp Xaa Xaa Xaa Xaa Xaa Xaa Xaa Tyr Gly Asp Ser Val
50 55 60

aaa gag cgc ttc gat atc cgt cgc gac aaa ggc tcc aac acc gtt acc 240
Lys Glu Arg Phe Asp Ile Arg Arg Asp Lys Gly Ser Asn Thr Val Thr
65 70 75 80

tta tcg atg gac gat ctg caa ccg gaa gac tct gca gaa tac aat tgt 288
Leu Ser Met Asp Asp Leu Gln Pro Glu Asp Ser Ala Glu Tyr Asn Cys
85 90 95

gca nnn nnn nnn nnn nnn nnn nnn nnn nnn nnn nnn nnn nnn nnn ggt 336
Ala Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Gly
100 105 110

cag ggt acc gac gtt acc gtc tcg tcg 363
Asn Gly Thr Asp Val Thr Val Ser Ser
115 120

<210> 24
<211> 121
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Exemplary primary scaffold

<220>
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<222> (25)..(33)
<223> The amino acid at each of positions 25-33 is unknown

<220>
<221> MISC_FEATURE
<222> (53)..(59)
<223> The amino acid at each of positions 53-59 is unknown

<220>
<221> MISC_FEATURE

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<222> (98)..(111)

<223> The amino acid at each of positions 98-111 is unknown

<400> 24

Asn Val Lys Leu Val Glu Lys Gly Gly Asn Phe Val Glu Asn Asp Asp
1 5 10 15

Asp Leu Lys Leu Thr Cys Arg Ala Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
20 25 30

Xaa Met Gly Trp Phe Arg Gln Ala Pro Asn Asp Asp Ser Thr Asn Val
35 40 45

Ala Thr Ile Asp Xaa Xaa Xaa Xaa Xaa Xaa Xaa Tyr Gly Asp Ser Val
50 55 60

Lys Glu Arg Phe Asp Ile Arg Arg Asp Lys Gly Ser Asn Thr Val Thr
65 70 75 80

Leu Ser Met Asp Asp Leu Gln Pro Glu Asp Ser Ala Glu Tyr Asn Cys
85 90 95

Ala Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Gly
100 105 110

Asn Gly Thr Asp Val Thr Val Ser Ser
115 120